



IFWO

RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/717,665

TIME: 11:38:38

Input Set : N:\Crif3\RULE60\10717665.raw

Output Set: N:\CRF4\08272004\J717665.raw

1 <110> APPLICANT: OriGene Technologies, Inc
 2 <120> TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
 3 <130> FILE REFERENCE: 1U 103 R1
 4 <140> CURRENT APPLICATION NUMBER: US/10/717,665
 5 <141> CURRENT FILING DATE: 2003-11-21
 6 <150> PRIOR APPLICATION NUMBER: US/10/164,595
 7 <151> PRIOR FILING DATE: 2002-06-10
 8 <160> NUMBER OF SEQ ID NOS: 80
 9 <170> SOFTWARE: PatentIn version 3.1
 11 <210> SEQ ID NO: 1
 12 <211> LENGTH: 5682
 13 <212> TYPE: DNA
 14 <213> ORGANISM: Homo sapiens
 15 <220> FEATURE:
 16 <221> NAME/KEY: CDS
 17 <222> LOCATION: (62)..(1195)
 18 <223> OTHER INFORMATION:

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 22 Met Glu Val Lys Pro Pro Pro Gly Arg Pro Gln Pro Asp Ser Gly Arg
 23 1 5 10 15
 24 cgc cgt cgc cgc cgg ggg gag gag ggc cat gat cca aag gaa cca gag 157
 25 Arg Arg Arg Arg Arg Gly Glu Glu Gly His Asp Pro Lys Glu Pro Glu
 26 20 25 30
 27 cag ttg aga aaa ctg ttt att ggt ggt ctg agc ttt gaa act aca gat 205
 28 Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu Thr Thr Asp
 29 35 40 45
 30 gat agt tta cga gaa cat ttt gag aaa tgg ggc aca ctc aca gat tgt 253
 31 Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly Thr Leu Thr Asp Cys
 32 50 55 60
 33 gtg gta atg aga gac ccc caa aca aaa cgt tcc agg ggc ttt ggt ttt 301
 34 Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly Phe Gly Phe
 35 65 70 75 80
 36 gtg act tat tct tgt gtt gaa gag gtg gat gca gca atg tgt gct cga 349
 37 Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala Ala Met Cys Ala Arg
 38 85 90 95
 39 cca cac aag gtt gat ggg cgt gta gtg gaa cca aag aga gct gtt tct 397
 40 Pro His Lys Val Asp Gly Arg Val Val Glu Pro Lys Arg Ala Val Ser
 41 100 105 110
 42 aga gag gat tct gta aag cct ggt gcc cat cta aca gtg aag aaa att 445
 43 Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu Thr Val Lys Lys Ile
 44 115 120 125

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45	ttt gtt ggt ggt att aaa gaa gat aca gaa gaa tat aat ttg aga gac	493
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48	tac ttt gaa aag tat ggc aag att gaa acc ata gaa gtt atg gaa gac	541
49	Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile Glu Val Met Glu Asp	
50	145 150 155 160	
51	agg cag agt gga aaa aag aga gga ttt gct ttt gta act ttt gat gat	589
52	Arg Gln Ser Gly Lys Lys Arg Gly Phe Ala Phe Val Thr Phe Asp Asp	
53	165 170 175	
54	cat gat aca gtt gat aaa att gtt gtt cag aaa tac cac act att aat	637
55	His Asp Thr Val Asp Lys Ile Val Val Gln Lys Tyr His Thr Ile Asn	
56	180 185 190	
57	ggg cat aat tgt gaa gtg aaa aag gcc ctt tct aaa caa gag atg cag	685
58	Gly His Asn Cys Glu Val Lys Lys Ala Leu Ser Lys Gln Glu Met Gln	
59	195 200 205	
60	tct gct gga tca cag aga ggt cgt gga ggt gga tct ggc aat ttt atg	733
61	Ser Ala Gly Ser Gln Arg Gly Arg Gly Gly Ser Gly Asn Phe Met	
62	210 215 220	
63	ggt cgc gga ggg aac ttt gga ggt ggt gga ggt aat ttt ggc cgt ggt	781
64	Gly Arg Gly Gly Asn Phe Gly Gly Gly Gly Asn Phe Gly Arg Gly	
65	225 230 235 240	
66	gga aac ttt ggt gga aga gga ggc tat ggt ggt gga ggt ggt ggc agc	829
67	Gly Asn Phe Gly Gly Arg Gly Gly Tyr Gly Gly Gly Gly Gly Gly Ser	
68	245 250 255	
69	aga ggt agt tat gga gga ggt gat ggt gga tat aat gga ttt gga ggt	877
70	Arg Gly Ser Tyr Gly Gly Gly Asp Gly Gly Tyr Asn Gly Phe Gly Gly	
71	260 265 270	
72	gat ggt ggc aac tat ggc ggt ggt cct ggt tat agt agt aga ggg ggc	925
73	Asp Gly Gly Asn Tyr Gly Gly Gly Pro Gly Tyr Ser Ser Arg Gly Gly	
74	275 280 285	
75	tat ggt ggt ggt gga cca gga tat gga aac caa ggt ggt gga tat ggt	973
76	Tyr Gly Gly Gly Gly Pro Gly Tyr Gly Asn Gln Gly Gly Gly Tyr Gly	
77	290 295 300	
78	gga ggt gga gga tat gat ggt tac aat gaa gga gga aat ttt ggc ggt	1021
79	Gly Gly Gly Gly Tyr Asp Gly Tyr Asn Glu Gly Gly Asn Phe Gly Gly	
80	305 310 315 320	
81	ggt aac tat ggt ggt ggt ggg aac tat aat gat ttt gga aat tat agt	1069
82	Gly Asn Tyr Gly Gly Gly Gly Asn Tyr Asn Asp Phe Gly Asn Tyr Ser	
83	325 330 335	
84	gga caa cag caa tca aat tat gga ccc atg aaa ggg ggc agt ttt ggt	1117
85	Gly Gln Gln Gln Ser Asn Tyr Gly Pro Met Lys Gly Gly Ser Phe Gly	
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87	gga aga agc tcg ggc agt ccc tat ggt ggt ggt tat gga tct ggt ggt	1165
88	Gly Arg Ser Ser Gly Ser Pro Tyr Gly Gly Gly Tyr Gly Ser Gly Gly	
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90	gga agt ggt gga tat ggt agc aga agg ttc taaaaacagc agaaaagggc	1215
91	Gly Ser Gly Gly Tyr Gly Ser Arg Arg Phe	
92	370 375	
93	tacagttctt agcaggagag agagcgagga gttgtcagga aagctgcagg ttactttgag	1275

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95	catagtcaga	aaagttactg	cagcttaaac	aggaaaccct	tcttggtcag	gactgtcata	1395
96	gccacagttt	gcaaaaagtg	cagctattga	ttaatgcaat	gtagtgtcaa	ttagatgtac	1455
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100	tgcagtttcg	aaggtgtttc	cttgtgagtt	aacaagtaaa	gaagatcatt	gttaattact	1695
101	attttgtatg	aattttgcta	aagttaactg	taaagaaaca	cctgctgact	tgcagtttaa	1755
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103	aatagataat	ttgtgtgttt	gcaatgtgtg	ttttagataa	ataggattgg	gtattttaat	1875
104	tagcatttgt	gaatttaata	gcattaagat	taccttcaaa	tgaaaaaaaa	tctcaaaatt	1935
105	tctatttggg	ttttgtgcat	tttcttttaa	aatgtaatca	tatgatttta	gtgtgttaga	1995
106	cttgctgagt	cctagctgtg	tttagaacat	ctctattcta	catttacctt	ggcctcattt	2055
107	gaactgctgc	cataggtttt	gggtgtaaag	aatgtttact	gccctccatt	taaattctga	2115
108	aaagggatgg	tggatgtttt	ccctctccta	cgtagaaaac	cattctttaa	aacttttgaa	2175
109	aatatagaac	cattaagcct	gctatatctg	agcaaattaa	tgggtacctt	ttttttctta	2235
110	tttaaagcac	aagaggccca	taaatcttga	gttactttta	attctttttt	ttgatacaag	2295
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112	tctgttttgt	attctataca	ttttgctgga	tgaaccaag	gatagttcag	gtataattgt	2415
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122	tccatttgtt	aatgggcata	tatgtgaaaa	gcagtgtaga	aaataggcta	atattagaaa	3015
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137	tgatttgcag	gttgaatgag	aaccctactt	gcctaaatga	ggaatgtctt	tcctaccatc	3915
138	taaaatacga	aggtttcttg	ctgggtaagg	tttgtagttg	acagtaaaac	ctgatgacac	3975
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141	cttagtttta	aaaattcccc	tgcgaaatag	ccataagtat	tcatatcaag	tcagttgtga	4155
142	ctccttgtgt	atacaattca	tttttgtgt	cttcagggta	aactcaattt	ttggtaaaagt	4215

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143 ggtttcagct tttgtgaaaa ccgtttttgt gtgtaagcat gacacacaac agactcagta 4275
144 agctgccccat cctcatacta ggaaaacacc ttcaaaggaa cattaanaagt taccagggcc 4335
145 aggcacagtg gctcacgcct gtaatcccag cactttggga ggctgaggca gatggatccc 4395
146 aagtccagga atttgagacg agcctgggca acatagttag agcctgtcaa caaaaaatag 4455
147 aaaaattagt tgggcttggt gatacacatc tgtagtccca gctatttggg aggctgcctt 4515
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150 ctcataagtt gtcttgcat taaattcagg gaattcattg gaccaatagg ttacattttc 4695
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152 aaaaacacat tttcccaaag aacactgaat taccgttcaa actggttggt gatgggtaat 4815
153 aagggtctgt tttgctgccc caaaagggtc taacaattta ggcggatagt ttacttaaaa 4875
154 aaaaaaatcc tttggagaca tactgaaaat gcaaactagt ttctaaatta tcaattccct 4935
155 acatgaagaa gcagtttgcc agagttagt ctcagaaaat gactgggttg ctctatttaa 4995
156 atcagaaccc aatttctacg cgtgttgaat aaggtaacag cctttgatga atttccttca 5055
157 caacatgggt ttagtgaagc aaacattttt tttttaaggg cattgttctt tctagtttat 5115
158 ttctttttat gaaataaaat tattttattt aaacagttcc attgtcgttt ctgaaaacta 5175
159 cagtattctc agaagttgta gcagcagtaa aaaaaaaaaa gttgttatat aagtgattgg 5235
160 ggcagattta actgattttg ttaaaccaat ttgtaagtta ctgcttctaa tattacactt 5295
161 ctaaaaagct gaatttatac tcatgtccta aaggagaata tgtggaata aagtatattt 5355
162 gttaaagtaac taattgaaat aggttggtt ttaagagttc cagtatataa taatcacaaa 5415
163 ttgaaacctg acagtatctt gggagttcca gtaatgtcac aaattagtga ataagcatgc 5475
164 cagtgtgcaa gggtaatgta aggattgtta gcctatctaa atattcaaaa ttactttaaa 5535
165 acttaagtat gttttctgat ttttaagaat tcagaagtgt tctgtaatgg attcagatgt 5595
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167 gaaatgtgaa aaaaaaaaaa aaaaaaa 5682

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169 <210> SEQ ID NO: 2

170 <211> LENGTH: 378

171 <212> TYPE: PRT

172 <213> ORGANISM: Homo sapiens

173 <400> SEQUENCE: 2

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178 Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu Thr Thr Asp
179 35 40 45
180 Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly Thr Leu Thr Asp Cys
181 50 55 60
182 Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly Phe Gly Phe
183 65 70 75 80
184 Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala Ala Met Cys Ala Arg
185 85 90 95
186 Pro His Lys Val Asp Gly Arg Val Val Glu Pro Lys Arg Ala Val Ser
187 100 105 110
188 Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu Thr Val Lys Lys Ile
189 115 120 125
190 Phe Val Gly Gly Ile Lys Glu Asp Thr Glu Glu Tyr Asn Leu Arg Asp
191 130 135 140
192 Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile Glu Val Met Glu Asp

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193      145      150      155      160
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195      165      170      175
196 His Asp Thr Val Asp Lys Ile Val Val Gln Lys Tyr His Thr Ile Asn
197      180      185      190
198 Gly His Asn Cys Glu Val Lys Lys Ala Leu Ser Lys Gln Glu Met Gln
199      195      200      205
200 Ser Ala Gly Ser Gln Arg Gly Arg Gly Gly Ser Gly Asn Phe Met
201      210      215      220
202 Gly Arg Gly Gly Asn Phe Gly Gly Gly Gly Gly Asn Phe Gly Arg Gly
203      225      230      235      240
204 Gly Asn Phe Gly Gly Arg Gly Gly Tyr Gly Gly Gly Gly Gly Gly Ser
205      245      250      255
206 Arg Gly Ser Tyr Gly Gly Gly Asp Gly Gly Tyr Asn Gly Phe Gly Gly
207      260      265      270
208 Asp Gly Gly Asn Tyr Gly Gly Gly Pro Gly Tyr Ser Ser Arg Gly Gly
209      275      280      285
210 Tyr Gly Gly Gly Gly Pro Gly Tyr Gly Asn Gln Gly Gly Gly Tyr Gly
211      290      295      300
212 Gly Gly Gly Gly Tyr Asp Gly Tyr Asn Glu Gly Gly Asn Phe Gly Gly
213      305      310      315      320
214 Gly Asn Tyr Gly Gly Gly Gly Asn Tyr Asn Asp Phe Gly Asn Tyr Ser
215      325      330      335
216 Gly Gln Gln Gln Ser Asn Tyr Gly Pro Met Lys Gly Gly Ser Phe Gly
217      340      345      350
218 Gly Arg Ser Ser Gly Ser Pro Tyr Gly Gly Gly Tyr Gly Ser Gly Gly
219      355      360      365
220 Gly Ser Gly Gly Tyr Gly Ser Arg Arg Phe
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223 <210> SEQ ID NO: 3

224 <211> LENGTH: 3985

225 <212> TYPE: DNA

226 <213> ORGANISM: Homo sapiens

227 <220> FEATURE:

228 <221> NAME/KEY: CDS

229 <222> LOCATION: (187)..(2529)

230 <223> OTHER INFORMATION:

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234 gccgccttcg ctctcacca tgtgtaaggc ggcggggagc cccgcctgag gtgcctaaa 180
235 cacact atg acc gct ccc gaa aag ccc gtg aaa caa gag gaa atg gct 228
236 Met Thr Ala Pro Glu Lys Pro Val Lys Gln Glu Glu Met Ala
237 1 5 10
238 gcc ttg gac gtg gat agc ggc ggc ggc ggt ggc ggc ggc ggc ggc cac 276
239 Ala Leu Asp Val Asp Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly His
240 15 20 25 30
241 ggc gag tat ctg cag cag cag caa cag cac gga aac ggt gcg gtg gcg 324
242 Gly Glu Tyr Leu Gln Gln Gln Gln Gln His Gly Asn Gly Ala Val Ala

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Input Set : N:\Crf3\RULE60\10717665.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; Xaa Pos. 162

Seq#:46; Xaa Pos. 162

VERIFICATION SUMMARY

DATE: 08/27/2004

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TIME: 11:38:40

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Output Set: N:\CRF4\08272004\J717665.raw

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L:1292 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:0
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